

APL-03-03-PCT-US SEQ LIST
SEQUENCE LISTING

<110> Aventis Pasteur Limited
Brunham, Robert
Raudonikiene, Ausra
Gallichan, Scott
Murdin, Andrew

<120> Immunization Against Chlamydia Infection

<130> APL-03-03-PCT-US

<140> 10/580,142

<141> 2006-05-19

<150> PCT/CA2004/002001

<151> 2004-11-19

<150> 60/481,690

<151> 2003-11-21

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<170> PatentIn version 3.3

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Leu Asn Ala Ala Gly Asn Gln Leu Gly Lys Thr Ser Asp Arg Leu Leu	
100 105 110	
ttc aaa gga tta aca gca cct cat cct att att cgc ttg gaa gct gct	384
Phe Lys Gly Leu Thr Ala Pro His Pro Ile Ile Arg Leu Glu Ala Ala	
115 120 125	
tac cgt ctg gcc tgt atg aaa aac agt aaa gta agt gac tac ctc tat	432
Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr Leu Tyr	
130 135 140	
tct ttt atc cac cag ctt cca gaa gaa atc caa aac tta gca gca acg	480
Ser Phe Ile His Gln Leu Pro Glu Glu Ile Gln Asn Leu Ala Ala Thr	
145 150 155 160	
att ttt ttg cag ctc gaa acg gaa gaa gca gat gct tat gtt cat aga	528
Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Val His Arg	
165 170 175	

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ctc	ctg	tct	tct	cct	aat	agt	cta	aca	aga	aac	tat	atg	gct	tat	cta	576
Leu	Leu	Ser	Ser	Pro	Asn	Ser	Leu	Thr	Arg	Asn	Tyr	Met	Ala	Tyr	Leu	
			180					185					190			
att	gga	gaa	tat	caa	cag	agg	aga	ttt	ctt	cca	acg	ctc	cgc	tcg	ttg	624
Ile	Gly	Glu	Tyr	Gln	Gln	Arg	Arg	Phe	Leu	Pro	Thr	Leu	Arg	Ser	Leu	
		195					200					205				
ctt	acc	agc	gca	gct	cct	tta	gac	caa	gaa	gga	tct	ttg	tat	gct	ata	672
Leu	Thr	Ser	Ala	Ala	Pro	Leu	Asp	Gln	Glu	Gly	Ser	Leu	Tyr	Ala	Ile	
	210					215					220					
gga	aaa	tta	gaa	gat	gcc	agc	agc	tat	cct	aaa	atc	aaa	gca	tta	agc	720
Gly	Lys	Leu	Glu	Asp	Ala	Ser	Ser	Tyr	Pro	Lys	Ile	Lys	Ala	Leu	Ser	
225					230					235					240	
tcc	aaa	tct	aac	cct	gaa	gtg	gct	ctt	gct	gct	gct	cag	aca	tta	tta	768
Ser	Lys	Ser	Asn	Pro	Glu	Val	Ala	Leu	Ala	Ala	Ala	Gln	Thr	Leu	Leu	
				245					250					255		
ttc	ttg	ggt	aaa	gaa	gat	gag	gct	ctt	cct	atc	cta	act	act	ttt	tgc	816
Phe	Leu	Gly	Lys	Glu	Asp	Glu	Ala	Leu	Pro	Ile	Leu	Thr	Thr	Phe	Cys	
			260					265					270			
cag	caa	gag	ctt	cct	cga	gct	att	tat	acc	tct	cgt	ttc	ctt	tca	tta	864
Gln	Gln	Glu	Leu	Pro	Arg	Ala	Ile	Tyr	Thr	Ser	Arg	Phe	Leu	Ser	Leu	
		275					280					285				
gaa	aaa	gga	gaa	gag	ctt	ctt	tta	ccc	atc	ttt	tgt	aaa	gct	att	aaa	912
Glu	Lys	Gly	Glu	Glu	Leu	Leu	Leu	Pro	Ile	Phe	Cys	Lys	Ala	Ile	Lys	
	290					295					300					
gaa	gaa	att	aaa	ctg	aat	gct	gct	ttg	gct	ctt	gtc	cac	ttg	gga	agc	960
Glu	Glu	Ile	Lys	Leu	Asn	Ala	Ala	Leu	Ala	Leu	Val	His	Leu	Gly	Ser	
305					310					315					320	
gtt	aat	cac	cta	gtg	ctt	agt	tat	tta	aca	gaa	ttt	tta	gaa	aat	aaa	1008
Val	Asn	His	Leu	Val	Leu	Ser	Tyr	Leu	Thr	Glu	Phe	Leu	Glu	Asn	Lys	
				325					330					335		
att	ctc	cac	cgc	ata	ttt	tta	ccc	acc	cat	tcg	ata	gga	aaa	gcc	acg	1056
Ile	Leu	His	Arg	Ile	Phe	Leu	Pro	Thr	His	Ser	Ile	Gly	Lys	Ala	Thr	
			340					345					350			
cag	ttt	tgg	aaa	gag	tgt	acg	gca	ctc	cct	ctt	cta	agc	cca	gaa	gaa	1104
Gln	Phe	Trp	Lys	Glu	Cys	Thr	Ala	Leu	Pro	Leu	Leu	Ser	Pro	Glu	Glu	
		355					360					365				
aaa	gca	aga	gct	ttg	gca	atg	tat	cgc	gca	gca	gaa	gat	acg	atc	ctc	1152
Lys	Ala	Arg	Ala	Leu	Ala	Met	Tyr	Arg	Ala	Ala	Glu	Asp	Thr	Ile	Leu	
	370					375					380					
tct	agt	tta	tta	aaa	tta	cct	aac	aat	gcc	tat	ctg	cct	tat	ttg	gaa	1200
Ser	Ser	Leu	Leu	Lys	Leu	Pro	Asn	Asn	Ala	Tyr	Leu	Pro	Tyr	Leu	Glu	
385					390					395					400	
cgt	att	cta	act	tca	caa	aaa	acc	cct	cta	gca	gct	aaa	gct	att	gct	1248
Arg	Ile	Leu	Thr	Ser	Gln	Lys	Thr	Pro	Leu	Ala	Ala	Lys	Ala	Ile	Ala	
				405					410					415		
ttt	tta	tca	gta	aca	gct	cat	cct	cag	gca	ctt	tct	tta	gtc	tcg	aaa	1296
Phe	Leu	Ser	Val	Thr	Ala	His	Pro	Gln	Ala	Leu	Ser	Leu	Val	Ser	Lys	

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420	425	430	
gca gca cta act cca gga gac cct atc att cgc gct tat gcg aat tta Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu 435 440 445			1344
gct tta tat aca atg acg caa gat cct gaa aag aaa gcc tta tta tat Ala Leu Tyr Thr Met Thr Gln Asp Pro Glu Lys Lys Ala Leu Leu Tyr 450 455 460			1392
caa tat gcc gaa cag tta ata gga gac acg att ttg ttt aca gat gag Gln Tyr Ala Glu Gln Leu Ile Gly Asp Thr Ile Leu Phe Thr Asp Glu 465 470 475 480			1440
gag aat ccc ctg cct tct ccc cat tct tcc tac ctg cga tat caa gtg Glu Asn Pro Leu Pro Ser Pro His Ser Ser Tyr Leu Arg Tyr Gln Val 485 490 495			1488
tcc cca gaa act cgt tct caa ctc atg cta act att tta gaa acc cta Ser Pro Glu Thr Arg Ser Gln Leu Met Ile Leu Thr Ile Leu Glu Thr Leu 500 505 510			1536
gtt tct tct aaa act gat gaa gac atc cga gtt ttt ctt tcg cta atg Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met 515 520 525			1584
aaa aaa acc cat tac aaa aat atc ccc atc tta tct gga tta tta atg Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met 530 535 540			1632
aga ata gtg gag cga gct cgg tac caa gct tac gta gaa caa aaa ctc Arg Ile Val Glu Arg Ala Arg Tyr Gln Ala Tyr Val Glu Gln Lys Leu 545 550 555 560			1680
atc tca gaa gag gat Ile Ser Glu Glu Asp 565			1695

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 <212> PRT
 <213> Chlamydia muridarum
 <400> 6

Met Cys Asp Phe Pro Pro Ser Val Ser Gln Lys Ile Leu Phe Leu Cys 1 5 10 15
Gln Lys Ser Ile Pro Gln Ala Leu Glu Ser Tyr Leu Glu Ala Ser Thr 20 25 30
Thr Tyr Gln Gln His Asn Phe Ser Ile Leu Arg Leu Ile Ala Lys Ser 35 40 45
Tyr Leu Gln Gln Ser Leu Phe Ser Glu Asp Ala Tyr Val Arg Lys Ser 50 55 60
Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Thr Leu Asp Leu

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75

65		70												80	
Leu	Ser	Glu	Ser	Ile	Glu	Thr	Gln	Asp	Leu	Tyr	Glu	Gln	Leu	Leu	Ile
				85					90					95	
Leu	Asn	Ala	Ala	Gly	Asn	Gln	Leu	Gly	Lys	Thr	Ser	Asp	Arg	Leu	Leu
			100					105					110		
Phe	Lys	Gly	Leu	Thr	Ala	Pro	His	Pro	Ile	Ile	Arg	Leu	Glu	Ala	Ala
		115					120					125			
Tyr	Arg	Leu	Ala	Cys	Met	Lys	Asn	Ser	Lys	Val	Ser	Asp	Tyr	Leu	Tyr
	130					135					140				
Ser	Phe	Ile	His	Gln	Leu	Pro	Glu	Glu	Ile	Gln	Asn	Leu	Ala	Ala	Thr
145					150					155					160
Ile	Phe	Leu	Gln	Leu	Glu	Thr	Glu	Glu	Ala	Asp	Ala	Tyr	Val	His	Arg
			165						170					175	
Leu	Leu	Ser	Ser	Pro	Asn	Ser	Leu	Thr	Arg	Asn	Tyr	Met	Ala	Tyr	Leu
			180					185					190		
Ile	Gly	Glu	Tyr	Gln	Gln	Arg	Arg	Phe	Leu	Pro	Thr	Leu	Arg	Ser	Leu
	195						200					205			
Leu	Thr	Ser	Ala	Ala	Pro	Leu	Asp	Gln	Glu	Gly	Ser	Leu	Tyr	Ala	Ile
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Gly	Lys	Leu	Glu	Asp	Ala	Ser	Ser	Tyr	Pro	Lys	Ile	Lys	Ala	Leu	Ser
225					230					235					240
Ser	Lys	Ser	Asn	Pro	Glu	Val	Ala	Leu	Ala	Ala	Ala	Gln	Thr	Leu	Leu
				245					250					255	
Phe	Leu	Gly	Lys	Glu	Asp	Glu	Ala	Leu	Pro	Ile	Leu	Thr	Thr	Phe	Cys
			260					265					270		
Gln	Gln	Glu	Leu	Pro	Arg	Ala	Ile	Tyr	Thr	Ser	Arg	Phe	Leu	Ser	Leu
		275					280					285			
Glu	Lys	Gly	Glu	Glu	Leu	Leu	Leu	Pro	Ile	Phe	Cys	Lys	Ala	Ile	Lys
	290					295					300				
Glu	Glu	Ile	Lys	Leu	Asn	Ala	Ala	Leu	Ala	Leu	Val	His	Leu	Gly	Ser
305					310					315					320

APL-03-03-PCT-US SEQ LIST

Val Asn His Leu Val Leu Ser Tyr Leu Thr Glu Phe Leu Glu Asn Lys
325 330 335

Ile Leu His Arg Ile Phe Leu Pro Thr His Ser Ile Gly Lys Ala Thr
340 345 350

Gln Phe Trp Lys Glu Cys Thr Ala Leu Pro Leu Leu Ser Pro Glu Glu
355 360 365

Lys Ala Arg Ala Leu Ala Met Tyr Arg Ala Ala Glu Asp Thr Ile Leu
370 375 380

Ser Ser Leu Leu Lys Leu Pro Asn Asn Ala Tyr Leu Pro Tyr Leu Glu
385 390 395 400

Arg Ile Leu Thr Ser Gln Lys Thr Pro Leu Ala Ala Lys Ala Ile Ala
405 410 415

Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys
420 425 430

Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu
435 440 445

Ala Leu Tyr Thr Met Thr Gln Asp Pro Glu Lys Lys Ala Leu Leu Tyr
450 455 460

Gln Tyr Ala Glu Gln Leu Ile Gly Asp Thr Ile Leu Phe Thr Asp Glu
465 470 475 480

Glu Asn Pro Leu Pro Ser Pro His Ser Ser Tyr Leu Arg Tyr Gln Val
485 490 495

Ser Pro Glu Thr Arg Ser Gln Leu Met Leu Thr Ile Leu Glu Thr Leu
500 505 510

Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met
515 520 525

Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met
530 535 540

Arg Ile Val Glu Arg Ala Arg Tyr Gln Ala Tyr Val Glu Gln Lys Leu
545 550 555 560

Ile Ser Glu Glu Asp
565

APL-03-03-PCT-US SEQ LIST

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 <212> DNA
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1 5 10 15	
cga aaa tca gtc cct caa gct cta gaa gcc tat ctc gaa gct tca gca	96
Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala Ser Ala	
20 25 30	
act tat caa caa cac gat ttc tcc gta tta cgc gta ata gca gaa tcg	144
Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala Glu Ser	
35 40 45	
tat tta caa caa agc ttt ctc tct gag gac acc tac ata cgt aaa agt	192
Tyr Leu Gln Gln Ser Phe Leu Ser Glu Asp Thr Tyr Ile Arg Lys Ser	
50 55 60	
gca att att gga gca ggg cta tct ggt tca tca gaa gct tta gag tta	240
Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Ala Leu Glu Leu	
65 70 75 80	
ctg tct gag gct ata gaa acg caa gat ctc tat gag caa cta ctc att	288
Leu Ser Glu Ala Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu Leu Ile	
85 90 95	
tta aat gct gca acc agc caa tta agc aaa act tct gac aaa ctt tta	336
Leu Asn Ala Ala Thr Ser Gln Leu Ser Lys Thr Ser Asp Lys Leu Leu	
100 105 110	
ttc aag gga tta aca gct tct cat cct gtc atc cgc tta gaa gct gct	384
Phe Lys Gly Leu Thr Ala Ser His Pro Val Ile Arg Leu Glu Ala Ala	
115 120 125	
tat cgt ctt gcc tgt atg aaa aat agc aag gta agt gat tac ctt tat	432
Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr Leu Tyr	
130 135 140	
tct ttt atc tac aag tta cca gaa gaa att caa aac cta gcg gca act	480
Ser Phe Ile Tyr Lys Leu Pro Glu Glu Ile Gln Asn Leu Ala Ala Thr	
145 150 155 160	
att ttc tta caa ctc gaa aca gaa gaa gct gat gct tat att cat cat	528
Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile His His	
165 170 175	
ttg ctc tct tct ccc aat aac ctg aca aga aac tat gtt gcc tat tta	576
Leu Leu Ser Ser Pro Asn Asn Leu Thr Arg Asn Tyr Val Ala Tyr Leu	
180 185 190	
att gga gag tac aaa caa aaa aga ttt ctt cca aca cta cgc tct tta	624
Ile Gly Glu Tyr Lys Gln Lys Arg Phe Leu Pro Thr Leu Arg Ser Leu	
195 200 205	

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ctt Leu	aca Thr 210	agt Ser	gcc Ala	tct Ser	cct Pro	tta Leu 215	gat Asp	caa Gln	gaa Glu	ggc Gly 220	gct Ala 220	ttg Leu	tat Tyr	gcg Ala	tta Leu	672
ggc Gly 225	aaa Lys	ctg Leu	gaa Glu	gac Asp	tct Ser 230	ggt Gly	agc Ser	tat Tyr	cct Pro	aga Arg 235	att Ile	aaa Lys	gct Ala	cta Leu	agc Ser 240	720
tct Ser	aga Arg	tcc Ser	aat Asn	cct Pro 245	gaa Glu	gta Val	gta Val	ctc Leu	gct Ala 250	gca Ala	gct Ala	cag Gln	aca Thr	tta Leu 255	tta Leu	768
ttc Phe	tta Leu	gag Glu	aaa Lys 260	gaa Glu	gaa Glu	gaa Glu	gct Ala	cta Leu 265	ccg Pro	atc Ile	cta Leu	acc Thr	aac Asn 270	ctt Leu	tgc Cys	816
caa Gln	caa Gln	aaa Lys 275	ctt Leu	ctt Leu	cga Arg	gcc Ala	ctg Leu 280	tat Tyr	acc Thr	gca Ala	cgt Arg	ttc Phe 285	ctc Leu	tcg Ser	caa Gln	864
gag Glu	aag Lys 290	ggt Gly	gaa Glu	gag Glu	ctt Leu	ctt Leu 295	ctt Leu	cca Pro	atc Ile	ttt Phe	tat Tyr 300	aac Asn	gca Ala	aca Thr	caa Gln	912
gaa Glu 305	gaa Glu	att Ile	aga Arg	ctg Leu	aat Asn 310	act Thr	gct Ala	tta Leu	gca Ala	ctt Leu 315	gtt Val	cat His	caa Gln	ggg Gly	tgt Cys 320	960
aca Thr	gat Asp	cct Pro	caa Gln	gtc Val 325	ctc Leu	cac His	tat Tyr	cta Leu	aca Thr 330	gaa Glu	atc Ile	tta Leu	gaa Glu	agt Ser 335	aaa Lys	1008
gtt Val	ctc Leu	cat His	cgc Arg 340	ata Ile	ttt Phe	tta Leu	cct Pro	act Thr 345	cac His	tcg Ser	aca Thr	gga Gly	aaa Lys 350	gct Ala	ata Ile	1056
cag Gln	ttc Phe	tgg Trp 355	aaa Lys	gaa Glu	tgc Cys	acc Thr	act Thr 360	ttt Phe	cct Pro	ctc Leu	atg Met	agc Ser 365	caa Gln	gaa Glu	gac Asp	1104
aaa Lys 370	atg Met	aga Arg	acg Thr	ttg Leu	gct Ala	atg Met 375	tat Tyr	cgg Arg	gta Val	gcg Ala	gaa Glu 380	gat Asp	acc Thr	atc Ile	ctc Leu	1152
tca Ser 385	gcg Ala	tta Leu	cta Leu	aaa Lys	tta Leu 390	ccc Pro	aat Asn	gac Asp	gcc Ala	tat Tyr 395	ctt Leu	cct Pro	tac Tyr	cta Leu	gag Glu 400	1200
cgc Arg	atc Ile	ctc Leu	gcc Ala	tca Ser 405	caa Gln	aaa Lys	act Thr	ata Ile	cta Leu 410	gca Ala	gct Ala	aaa Lys	gct Ala	att Ile 415	gct Ala	1248
ttt Phe	tta Leu	tcg Ser	gta Val 420	aca Thr	gct Ala	cat His	cct Pro	cag Gln 425	gca Ala	ctt Leu	tct Ser	tta Leu	gtc Val 430	tcg Ser	aaa Lys	1296
gct Ala	gca Ala	tta Leu 435	act Thr	cct Pro	gga Gly	gac Asp	cct Pro 440	atc Ile	att Ile	cgc Arg	gct Ala	tac Tyr 445	gct Ala	aat Asn	cta Leu	1344
gct Ala	tta Leu	tat Tyr	aca Thr	atg Met	acc Thr	aaa Lys	gat Asp	cct Pro	gag Glu	aaa Lys	aaa Lys	gct Ala	gtg Val	cta Leu	tac Tyr	1392

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450	455	460	
cga tat gct gaa caa tta ata gag gat acc att tta ttc aca gat gct Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr Asp Ala 465 470 475 480			1440
gaa aat ccg ctt ccc tct cca agc tct tct tat tta cgc tac caa gta Glu Asn Pro Leu Pro Ser Pro Ser Ser Tyr Leu Arg Tyr Gln Val 485 490 495			1488
tcc cct gag acc cgc aca caa ctt atg cta gct att ttg gaa acc tta Ser Pro Glu Thr Arg Thr Gln Leu Met Leu Ala Ile Leu Glu Thr Leu 500 505 510			1536
gtt tct tcc aaa acg gat gaa gat atc cgc gtt ttt ctt tcc cta atg Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met 515 520 525			1584
aaa aaa acc cat tac aaa aat atc ccg atc tta tca gga ttg tta atg Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met 530 535 540			1632
aga ata gtg gag Arg Ile Val Glu 545			1644

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 <212> PRT
 <213> Chlamydia trachomatis
 <400> 8

Met Cys Asp Phe Pro Ser Ser Val Ser Gln Arg Ile Leu Phe Ser Cys 1 5 10 15
Arg Lys Ser Val Pro Gln Ala Leu Glu Ala Tyr Leu Glu Ala Ser Ala 20 25 30
Thr Tyr Gln Gln His Asp Phe Ser Val Leu Arg Val Ile Ala Glu Ser 35 40 45
Tyr Leu Gln Gln Ser Phe Leu Ser Glu Asp Thr Tyr Ile Arg Lys Ser 50 55 60
Ala Ile Ile Gly Ala Gly Leu Ser Gly Ser Ser Glu Ala Leu Glu Leu 65 70 75 80
Leu Ser Glu Ala Ile Glu Thr Gln Asp Leu Tyr Glu Gln Leu Leu Ile 85 90 95
Leu Asn Ala Ala Thr Ser Gln Leu Ser Lys Thr Ser Asp Lys Leu Leu 100 105 110
Phe Lys Gly Leu Thr Ala Ser His Pro Val Ile Arg Leu Glu Ala Ala

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115

120

125

Tyr Arg Leu Ala Cys Met Lys Asn Ser Lys Val Ser Asp Tyr Leu Tyr
130 135 140

Ser Phe Ile Tyr Lys Leu Pro Glu Glu Ile Gln Asn Leu Ala Ala Thr
145 150 155 160

Ile Phe Leu Gln Leu Glu Thr Glu Glu Ala Asp Ala Tyr Ile His His
165 170 175

Leu Leu Ser Ser Pro Asn Asn Leu Thr Arg Asn Tyr Val Ala Tyr Leu
180 185 190

Ile Gly Glu Tyr Lys Gln Lys Arg Phe Leu Pro Thr Leu Arg Ser Leu
195 200 205

Leu Thr Ser Ala Ser Pro Leu Asp Gln Glu Gly Ala Leu Tyr Ala Leu
210 215 220

Gly Lys Leu Glu Asp Ser Gly Ser Tyr Pro Arg Ile Lys Ala Leu Ser
225 230 235 240

Ser Arg Ser Asn Pro Glu Val Val Leu Ala Ala Ala Gln Thr Leu Leu
245 250 255

Phe Leu Glu Lys Glu Glu Glu Ala Leu Pro Ile Leu Thr Asn Leu Cys
260 265 270

Gln Gln Lys Leu Leu Arg Ala Leu Tyr Thr Ala Arg Phe Leu Ser Gln
275 280 285

Glu Lys Gly Glu Glu Leu Leu Leu Pro Ile Phe Tyr Asn Ala Thr Gln
290 295 300

Glu Glu Ile Arg Leu Asn Thr Ala Leu Ala Leu Val His Gln Gly Cys
305 310 315 320

Thr Asp Pro Gln Val Leu His Tyr Leu Thr Glu Ile Leu Glu Ser Lys
325 330 335

Val Leu His Arg Ile Phe Leu Pro Thr His Ser Thr Gly Lys Ala Ile
340 345 350

Gln Phe Trp Lys Glu Cys Thr Thr Phe Pro Leu Met Ser Gln Glu Asp
355 360 365

APL-03-03-PCT-US SEQ LIST

Lys Met Arg Thr Leu Ala Met Tyr Arg Val Ala Glu Asp Thr Ile Leu
370 375 380

Ser Ala Leu Leu Lys Leu Pro Asn Asp Ala Tyr Leu Pro Tyr Leu Glu
385 390 395 400

Arg Ile Leu Ala Ser Gln Lys Thr Ile Leu Ala Ala Lys Ala Ile Ala
405 410 415

Phe Leu Ser Val Thr Ala His Pro Gln Ala Leu Ser Leu Val Ser Lys
420 425 430

Ala Ala Leu Thr Pro Gly Asp Pro Ile Ile Arg Ala Tyr Ala Asn Leu
435 440 445

Ala Leu Tyr Thr Met Thr Lys Asp Pro Glu Lys Lys Ala Val Leu Tyr
450 455 460

Arg Tyr Ala Glu Gln Leu Ile Glu Asp Thr Ile Leu Phe Thr Asp Ala
465 470 475 480

Glu Asn Pro Leu Pro Ser Pro Ser Ser Ser Tyr Leu Arg Tyr Gln Val
485 490 495

Ser Pro Glu Thr Arg Thr Gln Leu Met Leu Ala Ile Leu Glu Thr Leu
500 505 510

Val Ser Ser Lys Thr Asp Glu Asp Ile Arg Val Phe Leu Ser Leu Met
515 520 525

Lys Lys Thr His Tyr Lys Asn Ile Pro Ile Leu Ser Gly Leu Leu Met
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Arg Ile Val Glu
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41

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APL-03-03-PCT-US SEQ LIST

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